

Thu Sep 21 09:52:13 2000

us-09-508-238-4.rge

Page 16

TITLE Direct Submission
JOURNAL Submitted (27-NOV-1996) Biochemistry, University of Missouri, 117
Schweitzer Hall, Columbia, MO 65211, USA
FEATURES Location/Qualifiers
1.1931
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/db_xref="taxon:3888"
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7.1878
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QKRGDYTCCEYSGHGRCKINNGCNHNRKSHAFSLDGDGYKCCPAGTRGDYK
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CDS

BASE COUNT 555 a 306 c 518 g 552 t
ORIGIN

Query Match 77.4%; Score 17.8; DB 8; Length 1931;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 caggtatgtgattccaagtg 23
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Db 847 CAGCTATGTGTTCAGAGTG 867

RESULT 15
HS1013A10 112424 bp DNA HTG 08-MAR-2000
LOCUS Homo sapiens chromosome 6, clone RP5-1013A10 map p24.1-25.3, ***
DEFINITION SEQUENCING IN PROGRESS ***, in unordered pieces.
ACCESSION AL033383
VERSION AL033383.24 GI:5870348
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 112424)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (08-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
Cambs, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Sep 12, 1999 this sequence version replaced gi:5734384.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in
progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Contig_ID: 00741 Length: 112424p.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES

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Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Search completed: September 20, 2000, 08:24:58
Job time: 21038 sec

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CDS
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RESULT 14
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DEFINITION Pisum sativum BP-80 vacuolar sorting receptor mRNA, complete cds.
ACCESSION U79958
VERSION U79958.1 GI:1737221
KEYWORDS
SOURCE pea.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
Pisum.
REFERENCE 1 (bases 1 to 1931)
AUTHORS Kirsch,T., Paris,N., Butler,J.M., Beavers,L. and Rogers,J.C.
TITLE Purification and initial characterization of a potential plant
vacuolar targeting receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3403-3407 (1994)
MEDLINE 94211872
AUTHORS Paris,N., Rogers,S.W., Jiang,L., Kirsch,T., Beavers,L.,
Phillips,T.E. and Rogers,J.C.
TITLE Molecular cloning and further characterization of a probable plant
vacuolar sorting receptor
JOURNAL Plant Physiol. 115 (1), 29-39 (1997)
MEDLINE 97451769
REFERENCE 3 (bases 1 to 1931)
AUTHORS Paris,N., Rogers,S.W. and Rogers,J.C.

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81901 bp DNA sequencing in progress *** , in ordered

AC014473
AC014473.1
GI:6436862

Drosophila melanogaster; Hexapoda;
Arthropoda; Tracheata; Metazoa;
Insecta; Brachycera;

1 (bases 1 to 6190),
James M. and Yenter, J.C.

This sequence was identified in the database. Further information on this sequence e-mail to zhang@u.washington.edu.

* by the finished sequence

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/organism="Drosophila"
/ab xref="taxon:7227"

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84.06; pred. No. 41;
on 08;

b6 36832 CCL6994

DEFINITION Drosophila melanogaster strain Y; cn bw sp/02.G.21 map 90E-91A

ORGANISM
Drosophila melanogaster; Tracheata; neapoptosis;
Tularemia; Metazoa; Arthropoda; Brachycera;
Tularemia; Metazoa; Arthropoda; Brachycera;

AUTHORS
Celniker, S.E., Aggarwal, R., Chavez, C., Chew, M., Cieslik, M., Hoff, C., Champe, M., George, B.A., Harris, N.L., ...

Proscophila melanogaster
Rubin, G.M.

AUTHORS
CERNIGOI, J. / Chavez, C. /
Butenhoff, C. / Champe, M. /
George, R.A. / Harris, N.L. /
Galle, R. / Kearney, L. /

COMMENT On Sep 3, 1999 this sequence, including this sequence, further information about this sequence, visit our sequence

* as soon as possible
* be preserved.

	contig of 548 bp in length
5114	5741:
5194	

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27 18.4 92.0 2906 2 AF053968
28 18.4 92.0 2906 2 AF053968
29 18.4 92.0 2906 2 AF053968
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31 18.4 92.0 2906 2 AF053968
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ALIGNMENTS

RESULT 1
LOCUS A98413 20 bp DNA
DEFINITION Sequence 2 from Patent WO912949.
ACCESSION A98413
VERSION A98413.1 GI:6781514
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 20;
Pred. No. 6.8; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 gatagctgggtgtgaac 20
RESULT 2
LOCUS PARRN235 2893 bp DNA
DEFINITION Pseudomonas aeruginosa gene for 23S ribosomal RNA.
ACCESSION Y00432
VERSION Y00432.1 GI:45420
KEYWORDS 23S ribosomal RNA; ribosomal DNA.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
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Best Local Similarity 98.0%; Score 19.6; DB 2; Length 2906;
Pred. No. 5.3; Mismatches 1; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 gatagctgggtgtgaac 20

JOURNAL
Submitted (24-AUG-1987) Ulbrich N., Institut fuer Biochemie,
Fachbereich Chemie, Freie Universitaet Berlin, Otto-Hahn-Bau,
Thielallee 63, D-1000 Berlin 33 (Dahlem)
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 2893;
Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
LOCUS YE077925 2906 bp DNA
DEFINITION Yersinia enterocolitica 23S ribosomal RNA (rrl) gene, complete
sequence.
ACCESSION Y077925
VERSION Y077925.1 GI:3335033
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES
BASE COUNT
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Query Match
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Pred. No. 5.3; Mismatches 1; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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